SCORE Search Results Details for Application 10552515 and Search Result 20080624_135838_us-10-552-515-1_copy_157_933.rai.

This page gives you Search Results detail for the Application 10552515 and Search Result 20080624_135838_us-10-552-515-1_copy_157_933.rai.

Go Back to previous page

GenCore version 6.2.1

OM protein - protein search, using sw model

Run on: June 24, 2008, 15:22:38 ; Search time 279 Seconds
(without alignments)
518.704 Million cell updates/sec

Title: US-10-552-515-1_COPY_157_933
Perfect score: 4123
Sequence: 1 QQDVQDGNTTVHYALLSASW.....SELSSHWTPFTVPKASQLQQ 777

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1143754 seqs, 186252778 residues

Total number of hits satisfying chosen parameters: 1143754

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /ABSS/Data/CRF/ptodata/1/iaa/5_COMB.pep:*
2: /ABSS/Data/CRF/ptodata/1/iaa/6_COMB.pep:*
3: /ABSS/Data/CRF/ptodata/1/iaa/7_COMB.pep:*
4: /ABSS/Data/CRF/ptodata/1/iaa/H_COMB.pep:*
5: /ABSS/Data/CRF/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /ABSS/Data/CRF/ptodata/1/iaa/RE_COMB.pep:*
7: /ABSS/Data/CRF/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1502.5	36.4	920	2	US-10-104-047-2574	Sequence 2574, Ap
2	1154	28.0	596	2	US-10-104-047-2541	Sequence 2541, Ap
3	912.5	22.1	475	2	US-10-104-047-3116	Sequence 3116, Ap
4	873.5	21.2	642	3	US-10-108-260A-4483	Sequence 4483, Ap
5	796	19.3	425	2	US-09-270-767-45552	Sequence 45552, A
6	684.5	16.6	483	3	US-10-108-260A-3990	Sequence 3990, Ap
7	594.5	14.4	660	3	US-10-108-260A-3644	Sequence 3644, Ap
8	411.5	10.0	393	3	US-09-876-997-457	Sequence 457, App
9	411.5	10.0	393	3	US-10-643-836-457	Sequence 457, App
10	396.5	9.6	215	2	US-09-270-767-61064	Sequence 61064, A
11	329.5	8.0	366	2	US-09-270-767-32253	Sequence 32253, A
12	329.5	8.0	366	2	US-09-270-767-47470	Sequence 47470, A
13	290	7.0	189	2	US-09-270-767-31816	Sequence 31816, A
14	290	7.0	189	2	US-09-270-767-47033	Sequence 47033, A
15	255.5	6.2	199	2	US-09-270-767-31722	Sequence 31722, A
16	255.5	6.2	199	2	US-09-270-767-46939	Sequence 46939, A
17	186.5	4.5	166	2	US-09-621-976-4064	Sequence 4064, Ap
18	113.5	2.8	631	3	US-10-369-493-12179	Sequence 12179, A
19	108.5	2.6	523	2	US-09-949-016-11540	Sequence 11540, A
20	107.5	2.6	1107	3	US-11-216-782-11586	Sequence 11586, A
21	106.5	2.6	2013	1	US-08-324-977-12	Sequence 12, Appl
22	106.5	2.6	2013	1	US-08-384-616-12	Sequence 12, Appl
23	106.5	2.6	2013	1	US-08-904-686A-12	Sequence 12, Appl
24	106.5	2.6	2013	2	US-09-315-850-12	Sequence 12, Appl
25	106.5	2.6	3010	1	US-08-324-977-2	Sequence 2, Appli
26	106.5	2.6	3010	1	US-08-324-977-14	Sequence 14, Appl
27	106.5	2.6	3010	1	US-08-384-616-2	Sequence 2, Appli
28	106.5	2.6	3010	1	US-08-384-616-14	Sequence 14, Appl
29	106.5	2.6	3010	1	US-08-904-686A-2	Sequence 2, Appli
30	106.5	2.6	3010	1	US-08-904-686A-14	Sequence 14, Appl
31	106.5	2.6	3010	2	US-09-315-850-2	Sequence 2, Appli
32	106.5	2.6	3010	2	US-09-315-850-14	Sequence 14, Appl
33	106	2.6	539	2	US-09-248-796A-16542	Sequence 16542, A
34	105	2.5	1089	2	US-10-012-231A-102	Sequence 102, App
35	105	2.5	1089	2	US-10-015-389A-102	Sequence 102, App
36	105	2.5	1089	2	US-10-006-768A-102	Sequence 102, App
37	105	2.5	1089	2	US-10-015-671A-102	Sequence 102, App
38	105	2.5	1089	2	US-10-015-393A-102	Sequence 102, App
39	105	2.5	1089	2	US-10-011-833A-102	Sequence 102, App
40	105	2.5	1089	2	US-10-006-041A-102	Sequence 102, App
41	105	2.5	1089	2	US-10-012-064A-102	Sequence 102, App
42	105	2.5	1089	2	US-10-015-392A-102	Sequence 102, App
43	105	2.5	1089	3	US-10-011-795B-102	Sequence 102, App
44	105	2.5	1089	3	US-10-015-386A-102	Sequence 102, App
45	105	2.5	1089	3	US-10-012-121A-102	Sequence 102, App

ALIGNMENTS

RESULT 1
US-10-104-047-2574
; Sequence 2574, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2574
;   LENGTH: 920
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-104-047-2574

  Query Match   36.4%; Score 1502.5; DB 2; Length 920;
  Best Local Similarity   40.4%; Pred. No. 2e-150;
  Matches 328; Conservative 145; Mismatches 270; Indels   69; Gaps   20;

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Qy          8 NTTVHYALLSASWAVLCYYAEDLRLKLPLQE----LPNQASNWS------AGLLAWLGIP 57
              |: : :  | | | ||  ||| : :::| :     || :    |      : |  ||
Db        122 NSDIIFVKLHAPWEVLGRYAEQMNVRMPFRRKIYYLPRRYKFMSRIDKQISRLRRWLPKK 181

Qy         58 NVLL--EVVPDVPP-EYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGH 114
               : |  | :||:   : |:  |   ::  |:   |::||| :  | :|:  || :  |
Db        182 PMRLDKETLPDLEENDCYTAPFSQQRIHHFI-IHNKETFFNNATRSRIVHHILQRIKY-E 239

Qy        115 EKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQ 174
              | || :|:::||  |   ||||||:| :::          | | :|:: || || | |||
Db        240 EGKNKIGLNRLLTNGSYEAAFPLHEGSYRSKNSIRTHGAENHRHLLYECWASWGVWYKYQ 299

Qy        175 PLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDS 234
              ||| |||||||: |||||||:||| | ||| :|  ||| |   :     ::|:| : |
Db        300 PLDLVRRYFGEKIGLYFAWLGWYTGMLFPAAFIGLFVFLYGVTTLDHSQVSKEVCQATDI 359

Qy        235 FEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLA 293
                ||:|   |||  || :|  |:   |||:| ||||::|||:|| : ||:|||: | :|
Db        360 I-MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFFAVFMAVWATVFLEFWKRRRAVIA 418

Qy        294 YRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMV 352
              | ||  |:|: ||  |||| |  :     |||:|: |||     :  |::  :  |  |:
Db        419 YDWDLIDWEEEEEEIRPQFEAKYSKKERMNPISGKPEPYQAFTDKCSRLIVSASGIFFMI 478

Qy        353 AVVVMCLVSIILYRAIMAIVVSRSGNTLLA-AWA-----SRIASLTGSVV--NLVFILIL 404
               ||:  :  |::|| :         :|  |  ||     |::|: ||: |  |   |::|
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Db        479 CVVIAAVFGIVIYRVVTV-------STFAAFKWALIRNNSQVAT-TGTAVCINFCIIMLL 530

Qy        405 SKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNY 464
              : :|  :| :||  |  ||::::|::||||:|:|||||  ||  ||||| ||| |:|| |
Db        531 NVLYEKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNSSTFYIAFFLGRFTGHPGAY 590

Qy        465 HTLFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKR 523
                |    | |||   ||||:|  :: :||| ||  ||  |:  | :: || :   |  ::
Db        591 LRLINRWRLEECHPSGCLIDLCMQMGIIMVLKQTWNNFMELGYPLIQNWWTR---RKVRQ 647

Qy        524 KAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNW 581
              : |     |   || || | |    |||||||||:||||| |||||| ||||| |||||
Db        648 EHGPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQFGFTTIFVAAFPLAPLLALLNNI 707

Qy        582 VEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYR 641
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Db        708 IEIRLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITNAFVIAITSDFIPRLVYA 767

Qy        642 W----------TRAHDLRGFLNFTLA--------------RAPSSFAAAHNRTCRYRAFR 677
              :               : |::| :|:                  | |:    : |||| :|
Db        768 YKYGPCAGQGEAGQKCMVGYVNASLSVFRISDFENRSEPESDGSEFSGTPLKYCRYRDYR 827

Qy        678 DDDGH-----YSQTYWNLLAIRLAFVIVFEHVVFSVGRLLDLLVPDIPESVEIKVKREYY 732
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Db        828 DPPHSLVPYGYTLQFWHVLAARLAFIIVFEHLVFCIKHLISYLIPDLPKDLRDRMRREKY 887

Qy        733 LAKQALAENEVLFGTNGTKDEQPKGSELSSHW 764
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Db        888 LIQEMMYEAELERLQKERKERKKNGKAHHNEW 919


RESULT 2
US-10-104-047-2541
; Sequence 2541, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. 6943241el full length cDNA
;  FILE REFERENCE: H1-A0105
;  CURRENT APPLICATION NUMBER: US/10/104,047
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER:
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2541
;   LENGTH: 596
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-104-047-2541

  Query Match             28.0%;  Score 1154;  DB 2;  Length 596;
  Best Local Similarity   41.3%;  Pred. No. 1.7e-113;
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  Matches  250;  Conservative  108;  Mismatches  194;  Indels   54;  Gaps   14;

Qy        201 LLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAG 259
              | ||| :|  ||| |   :     ::|:| : |   |||:|   |||  || :|  |:
Db          2 LFPAAFIGLFVFLYGVTTLDHSQVSKEVCQATDII-MCPVCDKYCPFMRLSDSCVYAKVT 60

Qy        260 RLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAAS-APM 318
               |||:| ||||::|||:|| : ||:|||: | :|| ||  |:|: ||  |||| |  :
Db         61 HLFDNGATVFFAVFMAVWATVFLEFWKRRRAVIAYDWDLIDWEEEEEEIRPQFEAKYSKK 120

Qy        319 TAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGN 378
                 |||:|: |||     :  |::  :  |  |: ||:  :  |::|| :         :
Db        121 ERMNPISGKPEPYQAFTDKCSRLIVSASGIFFMICVVIAAVFGIVIYRVVTV-------S 173

Qy        379 TLLA-AWA-----SRIASLTGSVV--NLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDA 430
              |  |  ||     |::|: ||: |  |   |::|: :|  :| :||  |  ||::::|::
Db        174 TFAAFKWALIRNNSQVAT-TGTAVCINFCIIMLLNVLYEKVALLLTNLEQPRTESEWENS 232

Qy        431 FTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFG-VRNEECAAGGCLIELAQELL 489
              ||||:|:|||||  ||  ||||| ||| |:|| |  |    | |||   ||||:|  ::
Db        233 FTLKMFLFQFVNLNSSTFYIAFFLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCMQMG 292

Qy        490 VIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCE--G 547
              :||| ||  ||  |:  | :: || :   |  ::: |     |   || || | |    |
Db        293 IIMVLKQTWNNFMELGYPLIQNWWTR---RKVRQEHGPERKISFPQWEKDYNLQPMNAYG 349

Qy        548 LFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIG 607
              |||||||:|||||| |||||| ||||| ||||| :|||||| ||| ::|||:| ||:|||
Db        350 LFDEYLEMILQFGFTTIFVAAFPLAPLLALLNNIIEIRLDAYKFVTQWRRPLASRAKDIG 409

Qy        608 IWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRW----------TRAHDLRGFLNFTLA 657
              ||: || |:  |:||:|||::| :|||:||  | :               : |::| :|:
Db        410 IWYGILEGIGILSVITNAFVIAITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYVNASLS 469

Qy        658 --------------RAPSSFAAAHNRTCRYRAFRDDDGH-----YSQTYWNLLAIRLAFV 698
                           | |:    : |||| :||         |:  :|::|| ||||:
Db        470 VFRISDFENRSEPESDGSEFSGTPLKYCRYRDYRDPPHSLVPYGYTLQFWHVLAARLAFI 529

Qy        699 IVFEHVVFSVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGS 758
              |||||:|| :  |:  |:|||:|: :  :::|| || :: : | |:       |: :  |
Db        530 IVFEHLVFCIKHLISYLIPDLPKDLRDRMRREKYLIQEMMYEAELERLQKERKERKKNGK 589

Qy        759 ELSSHW 764
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Db        590 AHHNEW 595


RESULT 3
US-10-104-047-3116
; Sequence 3116, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
```

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;  TITLE OF INVENTION: No. 6943241el full length cDNA
;  FILE REFERENCE: H1-A0105
;  CURRENT APPLICATION NUMBER: US/10/104,047
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER:
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3116
;   LENGTH: 475
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-104-047-3116

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  Best Local Similarity   38.0%;  Pred. No. 7.2e-88;
  Matches  202;  Conservative   89;  Mismatches  143;  Indels   97;  Gaps   12;

Qy        274 MALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFP 333
              ||:|| : ||:|||: | :|| ||  |:|: |
Db          1 MAVWATVFLEFWKRRRAVIAYDWDLIDWEEEE---------------------------- 32

Qy        334 ERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLA-AWA-----SR 387
                              : ||:  :  |::|| :         :|  |  ||     |:
Db         33 ------------------ICVVIAAVFGIVIYRVVTV-------STFAAFKWALIRNNSQ 67

Qy        388 IASLTGSVV--NLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYS 445
              :|: ||: |  |   |::|: :|  :| :||  |  ||::::|::||||:|:|||||  |
Db         68 VAT-TGTAVCINFCIIMLLNVLYEKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNS 126

Qy        446 SPVYIAFFKGRFVGYPGNYHTLFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV 504
              |  ||||| ||| |:|| |  |    | |||   ||||:|  :: :||| ||  ||  |:
Db        127 STFYIAFFLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCMQMGIIMVLKQTWNNFMEL 186

Qy        505 LIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFV 562
                | :: || :   |  ::: |     |   || || | |    |||||||||:|||||
Db        187 GYPLIQNWWTR---RKVRQEHGPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQFGFT 243

Qy        563 TIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVI 622
              |||||| ||||| ||||| :|||||| ||| ::||||:| ||:|||||: || |:  |:||
Db        244 TIFVAAFPLAPLLALLNNIIEIRLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVI 303

Qy        623 SNAFLLAFSSDFLPRAYYRW----------TRAHDLRGFLNFTLA--------------R 658
              :|||::| :|||:||  | :               : |::| :|:
Db        304 TNAFVIAITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYVNASLSVFRISDFENRSEPES 363

Qy        659 APSSFAAAHNRTCRYRAFRDDDGH-----YSQTYWNLLAIRLAFVIVFEHVVFSVGRLLD 713
                | |:    : |||| :||         |:  :|::|| ||||:||||||:|| :  |:
Db        364 DGSEFSGTPLKYCRYRDYRDPPHSLVPYGYTLQFWHVLAARLAFIIVFEHLVFCIKHLIS 423

Qy        714 LLVPDIPESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHW 764
               |:||:|: :  :::|| || :: : | |:       |: :  |    : |
Db        424 YLIPDLPKDLRDRMRREKYLIQEMMYEAELERLQKERKERKKNGKAHHNEW 474
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RESULT 4
US-10-108-260A-4483
; Sequence 4483, Application US/10108260A
; Patent No. 7193069
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. 7193069el full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/10/108,260A
;  CURRENT FILING DATE:  2002-03-27
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4483
;   LENGTH: 642
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-108-260A-4483

  Query Match             21.2%;  Score 873.5;  DB 3;  Length 642;
  Best Local Similarity   39.2%;  Pred. No. 1.7e-83;
  Matches  192;  Conservative   93;  Mismatches  172;  Indels   33;  Gaps   11;

Qy          5 QDGNTTVH---YALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLL 61
              :| :| :|   :  : | | |||  || |:||:| ::: :   | : |||    | :||
Db        116 RDEDTKIHGVGFVKIHAPWNVLCREAEFLKLKMPTKKMYH--INETRGLLK--KINSVLQ 171

Qy         62 EVVPDVPPEYYSCR----------FRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTP 111
              ::   : |:    |          |   |   |  || :|:|| |  |  |::||| :|
Db        172 KITDPIQPKVAEHRPQTMKRLSYPFSREKQHLFDLSD-KDSFFDSKTRSTIVYEILKRTT 230

Qy        112 YGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWN 171
                  | : :||  ||| || :||:||||| :       :    | |::|:: |||:| :
Db        231 CTKAKYS-MGITSLLANGVYAAAYPLHDGDY-----NGENVEFNDRKLLYEEWARYGVFY 284

Qy        172 KYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS 231
              ||||:| ||:|||||: |||||| ||  |:||::|| :||| ||  :  :||: |:|
Db        285 KYQPIDLVRKYFGEKIGLYFAWLGVYTQMLIPASIVGIIVFLYGCATMDENIPSMEMCDQ 344

Qy        232 KDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSA 290
              : :  |||||   | :| :||||| |:|  |||:  |||||:||||||   :|:|||| 
Db        345 RHNITMCPLCDKTCSYWKMSSACATARASHLFDNPATVFFSVFMALWAATFMEHWKRKQM 404

Qy        291 TLAYRWDCSDYEDTEERPRPQFAA-----SAPMTAPNPITGEDEPYFPERSRARRMLAGS 345
               | |||| : :|: |: || :: |     |    : |  |  |:     | |    |
Db        405 RLNYRWDLTGFEEEEDHPRAEYEARVLEKSLKKESRNKET--DKVKLTWRDRFPAYLTNL 462

Qy        346 VVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILS 405
              | |: |:||    :: :|:||  ||  :: : :  : :      : |  ::||| |::|
Db        463 VSIIFMIAVTFAIVLGVIIYRISMAAALAMNSSPSVRSNIRVTVTATAVIINLVVIILLD 522

Qy        406 KIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYH 465
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              ::|  :|  ||: |: :|:  ||:    | |: :||| |:   |:|||||||| ||:|
Db        523 EVYGCIARWLTKIEVPKTEKSFEERLIFKAFLLKFVNSYTPIFYVAFFKGRFVGRPGDYV 582

Qy        466 TLF-GVRNEE 474
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Db        583 YIFRSFRMEE 592


RESULT 5
US-09-270-767-45552
; Sequence 45552, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45552
;   LENGTH: 425
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45552

  Query Match             19.3%;  Score 796;  DB 2;  Length 425;
  Best Local Similarity   41.1%;  Pred. No. 1.7e-75;
  Matches  171;  Conservative   85;  Mismatches  128;  Indels   32;  Gaps    9;

Qy        287 RKSATLAYRWDCSDYEDTEERPRPQFAA---SAPMTAPNPITGEDEPYFP-ERSRARRML 342
              | || : :||| : ::  || ||||: |     | |  : :|   ||  |  | :    :
Db          1 RYSAEITHRWDLTGFDVHEEHPRPQYLARLEHIPPTRVDYVTNIKEPTVPFWRMKLPATV 60

Qy        343 AGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFIL 402
                  |:::::|:  : |:::::||  |   :    : :  : |  :|: : : |||  :
Db         61 FSFSVVLLLIALAFVALLAVVVYRMSMLAALKVGASPMTTSSAIVLATASAAFVNLCLLY 120

Qy        403 ILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPG 462
              ||: :|  ||  ||  || ||||:|:|: |||::: ||||:|:|  |||||||:|||:||
Db        121 ILNYMYNHLAEYLTELEMWRTQTQFDDSLTLKIYLLQFVNYYASIFYIAFFKGKFVGHPG 180

Qy        463 NYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKK 522
               |: ||  | |||::|||| ||  :| :||||||  | : || :|    :|:|
Db        181 EYNKLFDYRQEECSSGGCLTELCIQLAIIMVGKQAFNTILEVYLPM---FWRKV----LA 233

Qy        523 RKAGASAGASQGP---------WEDDYELVP--CEGLFDEYLEMVLQFGFVTIFVAACPL 571
               : | |   :  |         |  |::|:     ||| ||||||||:||||||||| ||
Db        234 IQVGLSRLFNNTPNPDKTKDERWMRDFKLLDWGARGLFPEYLEMVLQYGFVTIFVAAFPL 293

Qy        572 APLFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFS 631
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              || |||||| :|:||||:| :  ::|||::| :|||:|: ||  :  |:||:| |::|||:
Db         294 APFFALLNNILEMRLDAKKLLTHHKRPVSQRVRDIGVWYRILDCIGKLSVITNGFIIAFT 353

Qy         632 SDFLPR-AYYRWTRAHDLRGFLNFTLAR-----APSSFAAAHN----RTCRYRAFR 677
              || :||   :   :   | |:||||||:      :|: :: | :     ||||  ||
Db         354 SDMIPRLVRHXVNKQGTLDGYLNFTLSEFKVIDSPTLYSLAGDLSNITTCRYTDFR 409


RESULT 6
US-10-108-260A-3990
; Sequence 3990, Application US/10108260A
; Patent No. 7193069
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. 7193069el full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/10/108,260A
;  CURRENT FILING DATE:  2002-03-27
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3990
;   LENGTH: 483
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-108-260A-3990

  Query Match             16.6%;  Score 684.5;  DB 3;  Length 483;
  Best Local Similarity   35.1%;  Pred. No. 1.7e-63;
  Matches  171;  Conservative   95;  Mismatches  168;  Indels   53;  Gaps   14;

Qy         323 PITGEDE--------PYFPERSRARRMLAGSVVIVVMVAVVVMCLV-----SIILYRAIM 369
              |   |:|        | :  |      |  :|::|  : ::::||:      :::|| :
Db           2 PAVSEEEMALQLINCPDYKLRPYQHSYLRSTVILV--LTLLMICLMIGMAHVLVVYRVLA 59

Qy         370 AIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFED 429
              : : | |    |    :    :||::|: | |:|::||   :|  |  :|| || :: |
Db          60 SALFSSSAVPFLEEQVTTAVVVTGALVHYVTIVIMTKINRRVALKLCDFEMPRTFSERES 119

Qy         430 AFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGV-RNEECAAGGCLIELAQEL 488
               ||:: |  ||   :|| :|||| || |:||    | |: : ||| | ||:::|  ::
Db         120 RFTIRFFTLQFFTHFSSLIYIAFILGRINGHPGKSTRLAGLWKLEECHASGCMMDLFVQM 179

Qy         489 LVIMVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGP----WEDDYELVP 544
               :||  || ::|  | |:|     |   : ||   :|  |    : |    |  :| | |
Db         180 AIIMGLKQTLSNCVEYLVP-----WVTHKCRS--LRASESGHLPRDPELRDWRRNYLLNP 232

Qy         545 CE--GLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVAER 602
                 ||||::||::|:|| |||||| ||||| || :| ||||||| | |   || |  :
Db         233 VNTFSLFDEFMEMMIQYGFTTIFVAAFPLAPLLALFSNLVEIRLDAIKMVWLQRRLVPRK 292

Qy         603 AQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRW----------TRAHDLRGFL 652
              |:||| |  :|  :  ||||:|  ::||:|:|:||  |::          :    |:|::
Db         293 AKDIGTWLQVLETIGVLAVIANGMVIAFTSEFIPRVVYKYRYSPCLKEGNSTVDCLKGYV 352
```

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Qy         653 NFTLA-------RAPSSFAAAHNRT-CRYRAFRD-DDGHYSQTYWNLLAIRLAFVIVFEH 703
               | :|:       : |     : | | |||| :|:  | ::|: :| ||||||||||:|||
Db         353 NHSLSVFHTKDFQDPDGIEGSENVTLCRYRDYRNPPDYNFSEQFWFLLAIRLAFVILFEH 412

Qy         704 VVFSVGRLLDLLVPDIPESVEIKV-KREYYLAKQALAENEVLFGTNGTKDEQPKGSELSS 762
               |   :  :    |||||:||: || : :|   :: :       |  |     |    : :
Db         413 VALCIKLIAAWFVPDIPQSVKNKVLEVKYQRLREKMWHGRQRLGGVGAGSRPP----MPA 468

Qy         763 HWTPFTV 769
               | || ::
Db         469 HPTPASI 475


RESULT 7
US-10-108-260A-3644
; Sequence 3644, Application US/10108260A
; Patent No. 7193069
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. 7193069el full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/10/108,260A
;  CURRENT FILING DATE:  2002-03-27
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3644
;   LENGTH: 660
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-108-260A-3644

  Query Match             14.4%;  Score 594.5;  DB 3;  Length 660;
  Best Local Similarity   24.1%;  Pred. No. 1.1e-53;
  Matches  171;  Conservative  122;  Mismatches  231;  Indels  185;  Gaps   20;

Qy          72 YSCRFRVNKLPRFLG-SDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLG--------- 121
               :: | | |    | |  || | | |  :   |:          || :||
Db         100 FTYRTRQN----FKGFDDNNDDFLTMAECQFII---------KHELENLRAKDEKMIPGY 146

Qy         122 -----------IHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHW-ARWGK 169
                        : :||  |::   |||||                  : |   |  |:
Db         147 PQAKLYPGKSLLRRLLTSGIVIQVFPLHDS-------------EALKKLEDTWYTRFAL 192

Qy         170 WNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELC 229
                 ||||:| :| |||| :|||| :| ::|  |:| ||:|
Db         193 --KYQPIDSIRGYFGETIALYFGFLEYFTFALIPMAVIG--------------------- 229

Qy         230 GSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKS 289
                           |::|              |:   | |: |  :|: ::|| |||
Db         230 --------------LPYYLFVWE----------DYDKYVIFASFNLIWSTVILELWKRGC 265

Qy         290 ATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIV 349
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              | : |||     :   | ||| |     :   | |||::|| :|   |  |:   |:  |
Db        266 ANMTYRWGTLLMKRKFEEPRPGFHG---VLGINSITGKEEPLYPSYKRQLRIYLVSLPFV 322

Qy        350 VMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYV 409
               :     : :: |     : |: :  :     : | | :     |::  : | |::::|
Db        323 CLCLYFSLYVMMIYFDMEVWALGLHENSG---SEWTS-VLLYVPSIIYAIVIEIMNRLYR 378

Qy        410 SLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFG 469
                 |  || || || :: :::   ||| :| |:| ::|  ||||
Db        379 YAAEFLTSWENHRLESAYQNHLILKVLVFNFLNCFASLFYIAFV---------------- 422

Qy        470 VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWW--QKFRLRSKKRKAGA 527
              ::: :          | | |  :::  |::| : |  :|    :|  :|  :| |::
Db        423 LKDMKL--------LRQSLATLLITSQILNQIMESFLP----YWLQRKHGVRVKRKVQAL 470

Qy        528 SAGASQGPWED---DYELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEI 584
               |      :|    : |:    | ||:|||: ||||:|::|    |||  ||:|||: |:
Db        471 KADIDATLYEQVILEKEMGTYLGTFDDYLELFLQFGYVSLFSCVYPLAAAFAVLNNFTEV 530

Qy        585 RLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTR 644
                 || |    ::|| :| : :||:|      :: ::|::|  |:  |       | :  ::
Db        531 NSDALKMCRVFKRPFSEPSANIGVWQLAFETMSVISVVTNCALIGMSPQV--NAVFPESK 588

Qy        645 AHDLRGFLNFTLARAPSSFAAAHNRTCRYRAFRDDDGHYSQTYWNLLAIRLAFVIVFEHV 704
              | ||                                                :  |:  ||
Db        589 A-DL-----------------------------------------------ILIVVAVEHA 601

Qy        705 VFSVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEVLFGTNGTKDE 753
              : ::  :|   :|| |  :::|: |  : : :|| : ::   |   |:|
Db        602 LLALKFILAFAIPDKPRHIQMKLARLEFESLEALKQQQMKLVTENLKEE 650
```

RESULT 8
US-09-876-997-457
; Sequence 457, Application US/09876997
; Patent No. 7060479
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/876,997
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/731,872
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 457

```
;   LENGTH: 393
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-876-997-457

  Query Match             10.0%;  Score 411.5;  DB 3;  Length 393;
  Best Local Similarity   23.8%;  Pred. No. 1.7e-34;
  Matches  111;  Conservative   95;  Mismatches  172;  Indels   89;  Gaps   11;

Qy        292 LAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVM 351
              : |||     :   | ||| |     :   | |||::|| :|   |  |:   |:  | :
Db          1 MTYRWGTLLMKRKFEEPRPGFHG---VLGINSITGKEEPLYPSYKRQLRIYLVSLPFVCL 57

Qy        352 VAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSL 411
                    : :: |     : |: :  :     : | | :     |::  : | |::::|
Db         58 CLYFSLYVMMIYFDMEVWALGLHENSG---SEWTS-VLLYVPSIIYAIVIEIMNRLYRYA 113

Qy        412 AHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVR 471
              |  || || || :: :::   ||| :| |:| ::|  ||||                 ::
Db        114 AEFLTSWENHRLESAYQNHLILKVLVFNFLNCFASLFYIAFV----------------LK 157

Qy        472 NEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWW--QKFRLRSKKRKAGASA 529
              : :         | | |  :::  |::| : |  :|    :|  :|  :| |::     |
Db        158 DMKL--------LRQSLATLLITSQILNQIMESFLP----YWLQRKHGVRVKRKVQALKA 205

Qy        530 GASQGPWED---DYELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRL 586
                   :|    : |:    | ||:|||: ||||:|::|    |||  ||:|||: |:
Db        206 DIDATLYEQVILEKEMGTYLGTFDDYLELFLQFGYVSLFSCVYPLAAAFAVLNNFTEVNS 265

Qy        587 DARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAH 646
              || |    ::|| :| : :||:|      :: ::|::|  |:  |      | :  ::|
Db        266 DALKMCRVFKRPFSEPSANIGVWQLAFETMSVISVVTNCALIGMSPQV--NAVFPESKA- 322

Qy        647 DLRGFLNFTLARAPSSFAAAHNRTCRYRAFRDDDGHYSQTYWNLLAIRLAFVIVFEHVVF 706
              ||                                          :  |:  || :
Db        323 DL----------------------------------------------ILIVVAVEHALL 336

Qy        707 SVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEVLFGTNGTKDE 753
              ::  :|   :|| |  :::|: |  : : :|| : ::   |   |:|
Db        337 ALKFILAFAIPDKPRHIQMKLARLEFESLEALKQQQMKLVTENLKEE 383


RESULT 9
US-10-643-836-457
; Sequence 457, Application US/10643836
; Patent No. 7271243
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, Jean Baptiste
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Jobert, Severin
;  TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
;  FILE REFERENCE: 78.US3.REG
;  CURRENT APPLICATION NUMBER: US/10/643,836
```

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;  CURRENT FILING DATE:  2003-08-19
;  PRIOR APPLICATION NUMBER: US/09/731,872
;  PRIOR FILING DATE: 2000-12-07
;  PRIOR APPLICATION NUMBER: US 60/169,629
;  PRIOR FILING DATE: 1999-12-08
;  PRIOR APPLICATION NUMBER: US 60/187,470
;  PRIOR FILING DATE: 2000-03-06
;  NUMBER OF SEQ ID NOS: 482
;  SOFTWARE: Patent.pm
; SEQ ID NO 457
;   LENGTH: 393
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-643-836-457

  Query Match             10.0%;  Score 411.5;  DB 3;  Length 393;
  Best Local Similarity   23.8%;  Pred. No. 1.7e-34;
  Matches  111;  Conservative   95;  Mismatches  172;  Indels   89;  Gaps   11;

Qy        292 LAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVM 351
              : |||     :   | ||| |     :   | |||::|| :|   |  |:   |:  | :
Db          1 MTYRWGTLLMKRKFEEPRPGFHG---VLGINSITGKEEPLYPSYKRQLRIYLVSLPFVCL 57

Qy        352 VAVVVMCLVSIILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSL 411
                   : :: |     : |: :  :     : | | :     |::  : | |::::|
Db         58 CLYFSLYVMMIYFDMEVWALGLHENSG---SEWTS-VLLYVPSIIYAIVIEIMNRLYRYA 113

Qy        412 AHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVR 471
              |  || || || :: :::   ||| :| |:| ::|  ||||                ::
Db        114 AEFLTSWENHRLESAYQNHLILKVLVFNFLNCFASLFYIAFV----------------LK 157

Qy        472 NEECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPKLKGWW--QKFRLRSKKRKAGASA 529
              : :         | | |  :::  |::| : |  :|    :|  :|  :| |::     |
Db        158 DMKL--------LRQSLATLLITSQILNQIMESFLP----YWLQRKHGVRVKRKVQALKA 205

Qy        530 GASQGPWED---DYELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRL 586
                   :|    : |:    | ||:|||: ||||:|::|    |||  ||:|||: |:
Db        206 DIDATLYEQVILEKEMGTYLGTFDDYLELFLQFGYVSLFSCVYPLAAAFAVLNNFTEVNS 265

Qy        587 DARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAH 646
              || |    ::|| :| : :||:|      :: ::|::|  |:  |      | :  ::|
Db        266 DALKMCRVFKRPFSEPSANIGVWQLAFETMSVISVVTNCALIGMSPQV--NAVFPESKA- 322

Qy        647 DLRGFLNFTLARAPSSFAAAHNRTCRYRAFRDDDGHYSQTYWNLLAIRLAFVIVFEHVVF 706
              ||                                          :  |:  || :
Db        323 DL----------------------------------------------ILIVVAVEHALL 336

Qy        707 SVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEVLFGTNGTKDE 753
              ::  :|   :|| |  :::|: |  : : :|| : ::   |   |:|
Db        337 ALKFILAFAIPDKPRHIQMKLARLEFESLEALKQQQMKLVTENLKEE 383


RESULT 10
```

```
US-09-270-767-61064
; Sequence 61064, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61064
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-61064

  Query Match             9.6%;  Score 396.5;  DB 2;  Length 215;
  Best Local Similarity   43.2%;  Pred. No. 2.6e-33;
  Matches   89;  Conservative   36;  Mismatches   54;  Indels   27;  Gaps    6;

Qy        492 MVGKQVINNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGASQGP---------WEDDYEL 542
              |||||  | : || :|    :|:|        : | |   :  |          |  |::|
Db          1 MVGKQAFNTILEVYLPM---FWRKV----LAIQVGLSRLFNNTPNPDKTKDERWMRDFKL 53

Qy        543 VP--CEGLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRRPVA 600
              :     ||| |||||||:|||||||| |||| |||||| :|:|||:| :  ::|||:
Db         54 LDWGARGLFPEYLEMVLQYGFVTIFVAAFPLAPFFALLNNILEMRLDAKKLLTHHKRPVS 113

Qy        601 ERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYRWTRAHDLRGFLNFTLAR-- 658
              :| :|||:|: ||  :  |:||:| |::||:|| :||      :   | |:||||||:
Db        114 QRVRDIGVWYRILDCIGKLSVITNGFIIAFTSDMIPRLVRHVNKQGTLDGYLNFTLSEFK 173

Qy        659 ---APSSFAAAHN----RTCRYRAFR 677
                 :|: :: | :     ||||  ||
Db        174 VIDSPTLYSLAGDLSNITTCRYTDFR 199


RESULT 11
US-09-270-767-32253
; Sequence 32253, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32253
;   LENGTH: 366
;   TYPE: PRT
```

```
;   ORGANISM: Drosophila melanogaster
US-09-270-767-32253

  Query Match             8.0%;  Score 329.5;  DB 2;  Length 366;
  Best Local Similarity   33.8%;  Pred. No. 8.7e-26;
  Matches   78;  Conservative   48;  Mismatches   86;  Indels   19;  Gaps    5;

Qy         11 VHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL------LEVV 64
              : :   : |    ||  ||| |:|::|::|:|  :    :    :  : :|       : |
Db        139 IWFVKIHAPLEVLRRYAEILKLRMPMKEIPGMSVVNRSTKSVFSSLKHVFQFFLRNIYVD 198

Qy         65 PDVPPEYYSCRFRV--NKLPRFLGSDNQDTFFTSTKRHQILFEIL--AKTPYGHEKKNLL 120
               :: |:  : ||    ::   :|    || |||:  | :|:  ||   : |  ::
Db        199 EEIFPK-RAHRFTAIYSRDKEYLFDIRQDCFFTTAVRSRIVEFILDRQRFPAKNQHDMAF 257

Qy        121 GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 180
              || :|:|||| |||:|||||                | :|::|||   || :||||| ::
Db        258 GIERLIAEGVYSAAYPLHDGEITETG--------TMRALLYKHWASVPKWYRYQPLDDIK 309

Qy        181 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS 231
               ||| |: |||||||:||  || |::|| : ||   | : : :| :::| |
Db        310 EYFGVKIGLYFAWLGYYTYMLLLASIVGVICFLYSWFSLKNYVPVKDICQS 360


RESULT 12
US-09-270-767-47470
; Sequence 47470, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47470
;   LENGTH: 366
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-47470

  Query Match             8.0%;  Score 329.5;  DB 2;  Length 366;
  Best Local Similarity   33.8%;  Pred. No. 8.7e-26;
  Matches   78;  Conservative   48;  Mismatches   86;  Indels   19;  Gaps    5;

Qy         11 VHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVL------LEVV 64
              : :   : |    ||  ||| |:|::|::|:|  :    :    :  : :|       : |
Db        139 IWFVKIHAPLEVLRRYAEILKLRMPMKEIPGMSVVNRSTKSVFSSLKHVFQFFLRNIYVD 198

Qy         65 PDVPPEYYSCRFRV--NKLPRFLGSDNQDTFFTSTKRHQILFEIL--AKTPYGHEKKNLL 120
               :: |:  : ||    ::   :|    || |||:  | :|:  ||   : |  ::
Db        199 EEIFPK-RAHRFTAIYSRDKEYLFDIRQDCFFTTAVRSRIVEFILDRQRFPAKNQHDMAF 257
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```
Qy         121 GIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVR 180
               || :|:|||| |||:|||||                 | :|::|||   || :||||| ::
Db         258 GIERLIAEGVYSAAYPLHDGEITETG--------TMRALLYKHWASVPKWYRYQPLDDIK 309

Qy         181 RYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS 231
                ||| |: |||||||:||  || |::|| : ||   | : : :| :::| |
Db         310 EYFGVKIGLYFAWLGYYTYMLLLASIVGVICFLYSWFSLKNYVPVKDICQS 360


RESULT 13
US-09-270-767-31816
; Sequence 31816, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31816
;   LENGTH: 189
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-31816

  Query Match             7.0%;  Score 290;  DB 2;  Length 189;
  Best Local Similarity   37.8%;  Pred. No. 5.1e-22;
  Matches   62;  Conservative   25;  Mismatches   59;  Indels   18;  Gaps    4;

Qy          93 FFTSTKRHQILFEILAKTPY--GHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQ 150
               |  :: |: |:  || :  :  | |  : ||| :|: :|| : |: |||
Db          39 FLDASTRYSIINFILQRQRFVEGEETADNLGIEKLVQDGVYTCAYTLHD---------- 87

Qy         151 APRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTL 210
                   : |  | : ||   ||   |||| :: ||| |||||||||||||  |:| :| | |
Db          88 ---KDDRDRLLKEWANISKWKNLQPLDQIKDYFGAKVALYFAWLGFYTQMLIPISVFGVL 144

Qy         211 VFLVGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSAC 253
                || |     ||  ::::|    :  ||| |   | :| |:  |
Db         145 CFLYGFITWNSDPISRDICDDNGTI-MCPQCDRSCDYWRLNETC 187


RESULT 14
US-09-270-767-47033
; Sequence 47033, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
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;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47033
;   LENGTH: 189
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-47033

  Query Match              7.0%;  Score 290;  DB 2;  Length 189;
  Best Local Similarity   37.8%;  Pred. No. 5.1e-22;
  Matches   62;  Conservative   25;  Mismatches   59;  Indels   18;  Gaps    4;

Qy         93 FFTSTKRHQILFEILAKTPY--GHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQ 150
                 |  :: |: |:  || :  :  | |  : ||| :|: :|| : |: |||
Db         39 FLDASTRYSIINFILQRQRFVEGEETADNLGIEKLVQDGVYTCAYTLHD----------- 87

Qy        151 APRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTL 210
                   : |  | : ||   ||   |||| :: ||| ||||||||||||  |:| :| | |
Db         88 ---KDDRDRLLKEWANISKWKNLQPLDQIKDYFGAKVALYFAWLGFYTQMLIPISVFGVL 144

Qy        211 VFLVGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSAC 253
                || |     ||  ::::|    :  ||| |   | :| |:  |
Db        145 CFLYGFITWNSDPISRDICDDNGTI-MCPQCDRSCDYWRLNETC 187


RESULT 15
US-09-270-767-31722
; Sequence 31722, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31722
;   LENGTH: 199
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-31722

  Query Match              6.2%;  Score 255.5;  DB 2;  Length 199;
  Best Local Similarity   29.8%;  Pred. No. 2.7e-18;
  Matches   59;  Conservative   46;  Mismatches   64;  Indels   29;  Gaps    5;

Qy        261 LFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTA 320
                | |:  || |:  ||:|||: ||:||| || | :||  : :    | ||||: |    |
Db         11 LIDNNMTVVFAFSMAIWAVVYLEFWKRYSAGLVHRWGLTGFTHHVEHPRPQYLARISRT- 69
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Qy         321 PNPITGEDEPYFPERSRARRMLAGSV---------------VIVVMVAVVVMCLVSIILY 365
                  : |  : |  :::  | :|   |                ::|: : : |: :  ||:|
Db          70 -KKLAG--KAYEQDQTGKRTILDPDVPFWSFKFLPNFTSYSIMVLFICISVIAIAGIIIY 126

Qy         366 RAIMAIVVSRSGNTLLAAWAS-----RIASLTGSVVNLVFILILSKIYVSLAHVLTRWEM 420
               |     :  |: :::| :  |      |  :|  :::|: | :|  :| :||  || :|
Db         127 R-----MAQRASHSILGSENSMTFKVMILPMTAGIIDLIVISLLDMVYSNLAVKLTNYEY 181

Qy         421 HRTQTKFEDAFTLKVFIF 438
                ||||:::::: |:| ::|
Db         182 CRTQTEYDESLTIKNYVF 199


Search completed: June 24, 2008, 15:27:19
Job time : 281 secs
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